



IFW16

## RAW SEQUENCE LISTING

DATE: 10/01/2004

PATENT APPLICATION: US/09/891,119B

TIME: 11:47:22

Input Set : A:\24577-cyb.ST25.txt

Output Set : N:\CRF4\10012004\I891119B.raw

3 <110> APPLICANT: Maddon, Paul J.  
 5 <120> TITLE OF INVENTION: DERIVATIVES OF SOLUBLE T-4  
 7 <130> FILE REFERENCE: 24577-CY-B  
 9 <140> CURRENT APPLICATION NUMBER: 09/891,119B  
 10 <141> CURRENT FILING DATE: 2001-06-25  
 12 <160> NUMBER OF SEQ ID NOS: 22  
 14 <170> SOFTWARE: PatentIn version 3.1  
 16 <210> SEQ ID NO: 1  
 17 <211> LENGTH: 1273  
 18 <212> TYPE: DNA  
 19 <213> ORGANISM: Human  
 21 <220> FEATURE:  
 22 <221> NAME/KEY: CDS  
 23 <222> LOCATION: (76)..(1257)  
 24 <223> OTHER INFORMATION:  
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 28 <221> NAME/KEY: CDS  
 29 <222> LOCATION: (1261)..(1269)  
 30 <223> OTHER INFORMATION:



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 34 caagcccaga gccctgccat ttctgtgggc tcaggtccct actgetcage ccccttccctcc 60  
 36 ctcggcaagg ccaca atg aac cgg gga gtc cct ttt agg cac ttg ctt ctg 111  
 37 Met Asn Arg Gly Val Pro Phe Arg His Leu Leu Leu  
 38 1 5 10  
 40 gtg ctg caa ctg gcg ctc ctc cca gca gcc act cag gga aag aaa gtg 159  
 41 Val Leu Gln Leu Ala Leu Leu Pro Ala Ala Thr Gln Gly Lys Lys Val  
 42 15 20 25  
 44 gtg ctg ggc aaa aaa ggg gat aca gtg gaa ctg acc tgt aca gct tcc 207  
 45 Val Leu Gly Lys Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser  
 46 30 35 40  
 48 cag aag aag agc ata caa ttc cac tgg aaa aac tcc aac cag ata aag 255  
 49 Gln Lys Lys Ser Ile Gln Phe His Trp Lys Asn Ser Asn Gln Ile Lys  
 50 45 50 55 60  
 52 att ctg gga aat cag ggc tcc tcc tta act aaa ggt cca tcc aag ctg 303  
 53 Ile Leu Gly Asn Gln Gly Ser Ser Leu Thr Lys Gly Pro Ser Lys Leu  
 54 65 70 75  
 56 aat gat cgc gct gac tca aga aga agc ctt tgg gac caa gga aac ttc 351  
 57 Asn Asp Arg Ala Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe  
 58 80 85 90  
 60 ccc ctg atc atc agg aat ctt aag ata gaa gac tca gat act tac atc 399  
 61 Pro Leu Ile Ile Arg Asn Leu Lys Ile Glu Asp Ser Asp Thr Tyr Ile  
 62 95 100 105  
 64 tgt gaa gtg gag gac cag aag gag gag gtg caa ttg cta gtg ttc gga 447

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65 Cys Glu Val Glu Asp Gln Lys Glu Glu Val Gln Leu Leu Val Phe Gly
66      110                      115                      120
68 ttg act gcc aac tct gac acc cac ctg ctt cag ggg cag agc ctg acc      495
69 Leu Thr Ala Asn Ser Asp Thr His Leu Leu Gln Gly Gln Ser Leu Thr
70 125                      130                      135                      140
72 ctg acc ttg gag agc ccc cct ggt agt agc ccc tca gtg caa tgt agg      543
73 Leu Thr Leu Glu Ser Pro Pro Gly Ser Ser Pro Ser Val Gln Cys Arg
74                      145                      150                      155
76 agt cca agg ggt aaa aac ata cag ggg ggg aag acc ctc tcc gtg tct      591
77 Ser Pro Arg Gly Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser Val Ser
78                      160                      165                      170
80 cag ctg gag ctc cag gat agt ggc acc tgg aca tgc act gtc ttg cag      639
81 Gln Leu Glu Leu Gln Asp Ser Gly Thr Trp Thr Cys Thr Val Leu Gln
82                      175                      180                      185
84 aac cag aag aag gtg gag ttc aaa ata gac atc gtg gtg cta gct ttc      687
85 Asn Gln Lys Lys Val Glu Phe Lys Ile Asp Ile Val Val Leu Ala Phe
86                      190                      195                      200
88 cag aag gcc tcc agc ata gtc tat aag aaa gag ggg gaa cag gtg gac      735
89 Gln Lys Ala Ser Ser Ile Val Tyr Lys Lys Glu Gly Glu Gln Val Asp
90 205                      210                      215                      220
92 ttc tcc ttc cca ctc gcc ttt aca gtt gaa aag ctg acg ggc agt ggc      783
93 Phe Ser Phe Pro Leu Ala Phe Thr Val Glu Lys Leu Thr Gly Ser Gly
94                      225                      230                      235
96 gag ctg tgg tgg cag gcg gag agg gct tcc tcc tcc aag tct tgg atc      831
97 Glu Leu Trp Trp Gln Ala Glu Arg Ala Ser Ser Ser Lys Ser Trp Ile
98                      240                      245                      250
100 acc ttt gac ctg aag aac aag gaa gtg tct gta aaa cgg gtt acc cag      879
101 Thr Phe Asp Leu Lys Asn Lys Glu Val Ser Val Lys Arg Val Thr Gln
102                      255                      260                      265
104 gac cct aag ctc cag atg ggc aag aag ctc ccg ctc cac ctc acc ctg      927
105 Asp Pro Lys Leu Gln Met Gly Lys Lys Leu Pro Leu His Leu Thr Leu
106                      270                      275                      280
108 ccc cag gcc ttg cct cag tat gct ggc tct gga aac ctc acc ctg gcc      975
109 Pro Gln Ala Leu Pro Gln Tyr Ala Gly Ser Gly Asn Leu Thr Leu Ala
110 285                      290                      295                      300
112 ctt gaa gcg aaa aca gga aag ttg cat cag gaa gtg aac ctg gtg gtg      1023
113 Leu Glu Ala Lys Thr Gly Lys Leu His Gln Glu Val Asn Leu Val Val
114                      305                      310                      315
116 atg aga gcc act cag ctc cag aaa aat ttg acc tgt gag gtg tgg gga      1071
117 Met Arg Ala Thr Gln Leu Gln Lys Asn Leu Thr Cys Glu Val Trp Gly
118                      320                      325                      330
120 ccc acc tcc cct aag ctg atg ctg agc ttg aaa ctg gag aac aag gag      1119
121 Pro Thr Ser Pro Lys Leu Met Leu Ser Leu Lys Leu Glu Asn Lys Glu
122                      335                      340                      345
124 gca aag gtc tcg aag cgg gag aag gcg gtg tgg gtg ctg aac cct gag      1167
125 Ala Lys Val Ser Lys Arg Glu Lys Ala Val Trp Val Leu Asn Pro Glu
126                      350                      355                      360
128 gcg ggg atg tgg cag tgt ctg ctg agt gac tcg gga cag gtc ctg ctg      1215
129 Ala Gly Met Trp Gln Cys Leu Leu Ser Asp Ser Gly Gln Val Leu Leu

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130 365          370          375          380
132 gaa tcc aac atc aag gtt ctg ccc aca tgg tcc acc ccg gtg taa tgg      1263
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134          385          390          395
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143 <212> TYPE: PRT
144 <213> ORGANISM: Human
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148 Met Asn Arg Gly Val Pro Phe Arg His Leu Leu Leu Val Leu Gln Leu
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152 Ala Leu Leu Pro Ala Ala Thr Gln Gly Lys Lys Val Val Leu Gly Lys
153          20          25          30
156 Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser Gln Lys Lys Ser
157          35          40          45
160 Ile Gln Phe His Trp Lys Asn Ser Asn Gln Ile Lys Ile Leu Gly Asn
161          50          55          60
164 Gln Gly Ser Ser Leu Thr Lys Gly Pro Ser Lys Leu Asn Asp Arg Ala
165 65          70          75          80
168 Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe Pro Leu Ile Ile
169          85          90          95
172 Arg Asn Leu Lys Ile Glu Asp Ser Asp Thr Tyr Ile Cys Glu Val Glu
173          100          105          110
176 Asp Gln Lys Glu Glu Val Gln Leu Leu Val Phe Gly Leu Thr Ala Asn
177          115          120          125
180 Ser Asp Thr His Leu Leu Gln Gly Gln Ser Leu Thr Leu Thr Leu Glu
181          130          135          140
184 Ser Pro Pro Gly Ser Ser Pro Ser Val Gln Cys Arg Ser Pro Arg Gly
185 145          150          155          160
188 Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser Val Ser Gln Leu Glu Leu
189          165          170          175
192 Gln Asp Ser Gly Thr Trp Thr Cys Thr Val Leu Gln Asn Gln Lys Lys
193          180          185          190
196 Val Glu Phe Lys Ile Asp Ile Val Val Leu Ala Phe Gln Lys Ala Ser
197          195          200          205
200 Ser Ile Val Tyr Lys Lys Glu Gly Glu Gln Val Asp Phe Ser Phe Pro
201          210          215          220
204 Leu Ala Phe Thr Val Glu Lys Leu Thr Gly Ser Gly Glu Leu Trp Trp
205 225          230          235          240
208 Gln Ala Glu Arg Ala Ser Ser Ser Lys Ser Trp Ile Thr Phe Asp Leu
209          245          250          255
212 Lys Asn Lys Glu Val Ser Val Lys Arg Val Thr Gln Asp Pro Lys Leu
213          260          265          270
216 Gln Met Gly Lys Lys Leu Pro Leu His Leu Thr Leu Pro Gln Ala Leu
217          275          280          285
220 Pro Gln Tyr Ala Gly Ser Gly Asn Leu Thr Leu Ala Leu Glu Ala Lys
221          290          295          300

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224 Thr Gly Lys Leu His Gln Glu Val Asn Leu Val Val Met Arg Ala Thr
225 305                      310                      315                      320
228 Gln Leu Gln Lys Asn Leu Thr Cys Glu Val Trp Gly Pro Thr Ser Pro
229                      325                      330                      335
232 Lys Leu Met Leu Ser Leu Lys Leu Glu Asn Lys Glu Ala Lys Val Ser
233                      340                      345                      350
236 Lys Arg Glu Lys Ala Val Trp Val Leu Asn Pro Glu Ala Gly Met Trp
237                      355                      360                      365
240 Gln Cys Leu Leu Ser Asp Ser Gly Gln Val Leu Leu Glu Ser Asn Ile
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244 Lys Val Leu Pro Thr Trp Ser Thr Pro Val Trp Arg Leu
245 385                      390                      395
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249 <211> LENGTH: 91
250 <212> TYPE: DNA
251 <213> ORGANISM: Artificial Sequence
253 <220> FEATURE:
254 <223> OTHER INFORMATION: OMPAST4
256 <400> SEQUENCE: 3
257 tatgaaaaag acagctatcg cgattgcagt ggcactggct gggttcgcta ccgtagcgca      60
259 ggccggctct agagtcgacc tagttaacta g                                     91
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264 <212> TYPE: DNA
265 <213> ORGANISM: Artificial Sequence
267 <220> FEATURE:
268 <223> OTHER INFORMATION: sk 727/725
270 <400> SEQUENCE: 4
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274 <210> SEQ ID NO: 5
275 <211> LENGTH: 48
276 <212> TYPE: DNA
277 <213> ORGANISM: Artificial Sequence
279 <220> FEATURE:
280 <223> OTHER INFORMATION: sk 727/725
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287 <211> LENGTH: 48
288 <212> TYPE: DNA
289 <213> ORGANISM: Artificial Sequence
291 <220> FEATURE:
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294 <400> SEQUENCE: 6
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299 <211> LENGTH: 48
300 <212> TYPE: DNA
301 <213> ORGANISM: Artificial Sequence

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313 <213> ORGANISM: Human
315 <400> SEQUENCE: 8
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320 ctggcgctcc tcccagcagc cactcagga aagaaagtgg tgcagggcaa aaaaggggat          180
322 acagtggaac tgacctgtac agcttcccag aagaagagca tacaattcca ctggaaaaac          240
324 tccaaccaga taaagattct gggaaatcag ggctccttct taactaaagg tccatccaag          300
326 ctgaatgata gcgctgactc aagaagaagc ctttgggacc aaggaaactt cccctgactc          360
328 atcaagaata ttaagataga agactcagat acttacatct gtgaagtgga ggaccagaag          420
330 gaggaggtgc aattgctagt gttcggattg actgccaact ctgacacca cctgcttcag          480
332 gggcagagcc tgacctgac cttggagagc cccctggta gtagccctc agtgcaatgt          540
334 aggagtccaa ggggtaaaaa catacagggg gggaagacc cctccgtgtc tcagctggag          600
336 ctccaggata gtggcacctg gacatgcact gtcttgaga accagaagaa ggtggagttc          660
338 aaaatagaca tcgtggtgct agcttcccag aaggcctcca gcatagtcta taagaaagag          720
340 ggggaacagg tggagttctc ctcccactc gcctttacag ttgaaaagct gacgggcagt          780
342 ggcgagctgt ggtggcaggc ggagagggct tctcctcca agtcttgat cacttttgac          840
344 ctgaagaaca aggaagtgtc tgtaaaacgg gttaccagc accctaagct ccagatgggc          900
346 aagaagctcc cgtccacct caccctgcc caggccttgc ctcaagtatgc tggctctgga          960
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350 gtgatgagag ccactcagct ccagaaaaat ttgacctgtg aggtgtgggg acccacctcc          1080
352 cctaagctga tgcctgagctt gaaactggag aacaaggagg caaagggttc gaagcgggag          1140
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362 aagagactcc tcagtgaaga gaagacctgc cagtgccttc accggtttca gaagacatgt          1440
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366 ccgcgtttcc tgccctgcga ccagatgaat gtagcagatc ccacgctctg gcctcctgtt          1560
368 cgtcctccct acaatttgcc attgtttctc ctgggttagg ccccggttc actggttgag          1620
370 tgttgctctc tagtttccag aggttaatac acaccgtcct ccacgccatt tccttttct          1680
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378 <211> LENGTH: 457
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380 <213> ORGANISM: human
382 <400> SEQUENCE: 9
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389          20          25          30
392 Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser Gln Lys Lys Ser

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**VERIFICATION SUMMARY**

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Input Set : A:\24577-cyb.ST25.txt

Output Set: N:\CRF4\10012004\I891119B.raw

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L:33 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:30